46

#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/055,145A

DATE: 10/26/98 TIME: 11:25:12

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This Raw Listing contains the General Information Section and up to the first pages.

ENTERED SEQUENCE LISTING 1 2 General Information: 3 (1) 5 (i) APPLICANT: Weeks, Donald P. 6 Wang, Xiao-Zhuo Herman, Patricia L. 7 8 9 (ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS" 10 11 (iii) NUMBER OF SEQUENCES: 6 12 RECEIVED 13 14 (iv) CORRESPONDENCE ADDRESS: 15 (A) ADDRESSEE: Sheridan Ross P.C. 16 (B) STREET: 1700 Lincoln St., Suite 3500 17 (C) CITY: Denver TECH CENTER 1600/2900 (D) STATE: Colorado 18 19 (E) COUNTRY: USA 20 (F) ZIP: 80203 21 22 (v) COMPUTER READABLE FORM: 23 (A) MEDIUM TYPE: Floppy disk 24 (B) COMPUTER: IBM PC compatible 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 27 (vi) CURRENT APPLICATION DATA: 28 (A) APPLICATION NUMBER: 29 30 (B) FILING DATE: 31 (C) CLASSIFICATION: 32 33 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/042,666 34 35 (B) FILING DATE: 04-APR-1997 36 37 (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 60/042,941 38 39 (B) FILING DATE: 04-APR-1997 40 41 (viii) ATTORNEY/AGENT INFORMATION: 42 (A) NAME: Crook, Wannell M. 43 (B) REGISTRATION NUMBER: 31,071 44 (C) REFERENCE/DOCKET NUMBER: 3553-18 45

(ix) TELECOMMUNICATION INFORMATION:

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/055,145A

DATE: 10/26/98 TIME: 11:25:13

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47	(A) TELEPHONE: (303) 863-9700	
48	(B) TELEFAX: (303) 863-0223	
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50		
51 52	(2) INFORMATION FOR SEQ ID NO:1:	
52 53	(i) CECHENCE CUADACTEDISTICS.	
53 54	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 29 amino acids</li></ul>	
55	(B) TYPE: amino acid	
56	(C) STRANDEDNESS: single	
57	(D) TOPOLOGY: linear	
58	(2) 10102011 1211041	
59	(ii) MOLECULE TYPE: protein	
60	(, <u>-</u>	
61		
62	(ix) FEATURE:	
63	(A) NAME/KEY: Region	
64	(B) LOCATION: 28	
65	(D) OTHER INFORMATION: /note= "Best guess for	Xaa = Asp or
66	Thr"	
67		
68	(ix) FEATURE:	
69	(A) NAME/KEY: Region	
70	(B) LOCATION: 29	v
71	(D) OTHER INFORMATION: /note= "Best guess for	xaa = Pro"
72		
73 74	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
7 <b>4</b> 75	(XI) SEQUENCE DESCRIPTION. SEQ ID NO.1.	
76	Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro	Glu Glu Leu
77	1 5 10	15
78		<del>-</del> -
79	Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa	
80	20 25	
81		
82	(2) INFORMATION FOR SEQ ID NO:2:	
83		
84	(i) SEQUENCE CHARACTERISTICS:	
85	(A) LENGTH: 20 amino acids	
86	(B) TYPE: amino acid	
87	(C) STRANDEDNESS: single	
88	(D) TOPOLOGY: linear	
89	(ii) NOI BOULE MUDE, montain	
90 91	(ii) MOLECULE TYPE: protein	
92		
93	(ix) FEATURE:	
94	(A) NAME/KEY: Region	
95	(B) LOCATION: 8	
96	(D) OTHER INFORMATION: /note= "Best guess for	Xaa = Cys"
97		•
98	(ix) FEATURE:	
99	(A) NAME/KEY: Region	

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/055,145A

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111			(1	D) 05	THER	INF	ORMA'	rion	: /n	ote=	"Be:	st gi	uess	for	Xaa	= Cy	's"	
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126				3) T										15			•	
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127 128			((	2) S.	ranı		ESS:	sing								i mozer	· (a):	
127 128 129			(1	C) S.	TRANI OPOL(	DEDNI DGY:	ESS: line	sinq ear								i rooger	· ''O';	
127 128		(ii)	(1	C) S.	TRANI OPOL(	DEDNI	ESS: line	sinq ear								i magazi	· W	
127 128 129		(ii)	(1	C) S.	TRANI OPOL(	DEDNI DGY:	ESS: line	sinq ear								i sugar	· (20)	
127 128 129 130		(ii)	(1	C) S.	TRANI OPOL(	DEDNI DGY:	ESS: line	sinq ear								t rough	· V	
127 128 129 130 131			() (1 ) MOI	C) STOD) TO	TRANI OPOLO	DEDNI DGY:	ESS: line	sinq ear								i su <sub>gar</sub>	· W	
127 128 129 130 131 132 133			(( (1 ) MO1 ) FE	C) ST D) TO LECUI	TRANI OPOLO LE TY	DEDNI DGY: YPE:	ESS: line cDN	sinq ear								<sup>ter</sup> wy s	· W	
127 128 129 130 131 132 133			(() (1) ) MOI ) FE	C) ST D) TO LECUI ATURI A) NA	TRANI DPOLO LE TY E: AME/I	DEDNI DGY: YPE: KEY:	ESS: line CDNA	sing ear A								t congre	· W	
127 128 129 130 131 132 133 134 135			(() (1) ) MOI ) FE	C) ST D) TO LECUI ATURI A) NA	TRANI DPOLO LE TY E: AME/I	DEDNI DGY: YPE:	ESS: line CDNA	sing ear A								t enge	· W	
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127 128 129 130 131 132 133 134 135 136 137		(ix)	(() (1) () MOI () FEA ()	C) ST D) TO LECUI ATURI A) NA B) LO	TRANI DPOLO LE TY  E: AME/I DCAT	DEDNI DGY: YPE: KEY: ION:	CDS	sing ear A	gle		0.2.					<sup>Fer</sup> uge	· 'W'	
127 128 129 130 131 132 133 134 135 136 137		(ix)	(() (1) () MOI () FEA ()	C) ST D) TO LECUI ATURI A) NA B) LO	TRANI DPOLO LE TY  E: AME/I DCAT	DEDNI DGY: YPE: KEY:	CDS	sing ear A	gle	ID N	O:3:					1 · cu <sub>p</sub> ,	· 'W'	
127 128 129 130 131 132 133 134 135 136 137 138		(ix)	(() (1) () MOI () FEA (1) (1) () SEQ	C) STOD) TO	TRANI DPOLO LE TY  E: AME/I DCAT:	DEDNI DGY: YPE: KEY: ION:	CDS	singear A	gle SEQ :							1 · cu <sub>gʻ</sub> ;	· W	
127 128 129 130 131 132 133 134 135 136 137 138 139 140		(ix)	(() (1) MOI ) FEA (1) (1) SEC	C) STOD) TO	TRANIC POLO LE TY E: AME/I DCAT: CE DI	DEDNI DGY: YPE: KEY: ION: ESCR:	CDNACCDS	singear A 1020 DN: :	gle SEQ :	GTG	GCG		CTG	ccc	GAG	GAA	· W	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140		(ix)	(() (1) MOI ) FEA (1) (1) SEC	C) STOD) TO	TRANIC POLO LE TY E: AME/I DCAT: CE DI	DEDNI DGY: YPE: KEY: ION: ESCR:	CDNACCDS	singear A 1020 DN: :	gle SEQ :	GTG			CTG	ccc	GAG	GAA	· W	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140		(ix)	(() (1) () MOI () FEA (1) (1) () SEQ TTC	C) STOD) TO	TRANIC POLO LE TY E: AME/I DCAT: CE DI	DEDNI DGY: YPE: KEY: ION: ESCR:	CDNACCDS	singear A 1020 DN: :	gle SEQ :	GTG	GCG		CTG	ccc	GAG	GAA	· W	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140	Met	(ix)	(() (1) () MOI () FEA (1) (1) () SEQ TTC	C) STOD) TO	TRANICE TY  E: AME/I CE DI  CGC Arg	DEDNI DGY: YPE: KEY: ION: ESCR:	CDNACCDS	singear A 1020 DN: :	gle SEQ :	GTG Val	GCG		CTG	ccc	GAG Glu	GAA	· ·w·	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143	Met 1	(ix) (xi) ACC	) MOI ) FEA (1) ) SEC TTC Phe	C) STOD TO	TRANIC CE DI CGC Arg 5	DEDNI DGY: YPE: KEY: ION: ESCR: AAT Asn	CDNA  CDS  LOTIC  CDS  CDS  CDS  CDS  CDS  CDS  CDS  C	sing ear 1020 ON: :	SEQ : TAT Tyr	GTG Val 10	GCG Ala	Ala	CTG Leu	CCC Pro	GAG Glu 15	GAA Glu	· W	48
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	Met 1 CTG	(ixi) ACC Thr	) MOI ) FEA (1) ) SEC TTC Phe	C) STOD TO	TRANIC CE TY  CE DI  CGC  Arg  5  CCG	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASn	CDNA  CDS  LPTIC  GCC  Ala	singear A 1020 ON: : TGG Trp	SEQ : TAT Tyr	GTG Val 10	GCG Ala	Ala	CTG Leu ACA	CCC Pro	GAG Glu 15 CTC	GAA Glu GCG	· W	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	Met 1 CTG	(ixi) ACC Thr	) MOI ) FEA (1) ) SEC TTC Phe	C) STOD TO	TRANIC CE TY  CE DI  CGC  Arg  5  CCG	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASn	CDNA  CDS  LPTIC  GCC  Ala  GGC	sing ear 1020 ON: : TGG Trp	SEQ TAT Tyr ACG Thr	GTG Val 10	GCG Ala	Ala	CTG Leu ACA	CCC Pro	GAG Glu 15 CTC	GAA Glu GCG	·	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146	Met 1 CTG	(ixi) ACC Thr	) MOI ) FEA (1) ) SEC TTC Phe	C) STOD TO	TRANIC CE TY  CE DI  CGC  Arg  5  CCG	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASn	CDNA  CDS  LPTIC  GCC  Ala  GGC	sing ear 1020 ON: : TGG Trp	SEQ : TAT Tyr	GTG Val 10	GCG Ala	Ala	CTG Leu ACA	CCC Pro	GAG Glu 15 CTC	GAA Glu GCG	·	
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	Met l CTG Leu	(ix) (xi) ACC Thr TCC ser	() () () () () () () () () () () () () (	C) STOD TO	E: AME/I CE DI CGC Arg CCG Pro	DEDNI DGY: YPE: KEY: ION: ESCR: AAT Asn CTC Leu	CDNA  CDS  1  IPTIC  GCC  Ala  GGC  Gly	sing ear A 1020 DN: : TGG Trp CGG Arg	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	·	96
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	Met 1 CTG Leu	(ix) (xi) ACC Thr TCC ser	() () () () () () () () () () () () () (	C) STOD TO	E: AME/I CE DI CGC Arg CCG Pro	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASN CTC Leu	CDS CDNA CDS 1	sing ear A 1020 DN: : TGG Trp CGG Arg	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30 GAC	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	·	
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127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	Met 1 CTG Leu	(ix) (xi) ACC Thr TCC ser	() () () () () () () () () () () () () (	C) STOD TO	E: AME/I CE DI CGC Arg CCG Pro	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASN CTC Leu	CDS CDNA CDS 1	sing ear A 1020 DN: : TGG Trp CGG Arg	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30 GAC	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	· W	96
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	Met 1 CTG Leu	(ix) (xi) ACC Thr TCC ser	() () () () () () () () () () () () () (	C) STOD TO	E: AME/I CE DI CGC Arg CCG Pro	DEDNI DGY: YPE: KEY: ION: ESCR: AAT ASN CTC Leu	CDS CDNA CDS 1	singear A 1020 DN: : TGG Trp CGG Arg GTG Val	SEQ TAT Tyr ACG Thr 25	GTG Val 10 ATT Ile	GCG Ala CTC Leu	Ala GAC Asp	CTG Leu ACA Thr	CCC Pro CCG Pro 30 GAC	GAG Glu 15 CTC Leu	GAA Glu GCG Ala	· W	96
127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151	Met 1 CTG Leu CTC Leu	(ix) (xi) ACC Thr TCC Ser TAC Tyr	() () () () () () () () () () () () () (	C) STO TO T	E: AME/IDCATI CE DI CGC Arg CCG Pro	DEDNI DGY: YPE: XEY: ION: ESCRI AAT ASN CTC Leu GAC ASP	CDS CDNA CDS 1	singear A 1020 DN: S TGG Trp CGG Arg GTG Val 40	SEQ TAT Tyr ACG Thr 25 GTC Val	GTG Val 10 ATT Ile GCG Ala	GCG Ala CTC Leu	Ala GAC Asp CTG Leu	CTG Leu ACA Thr CTC Leu 45	CCC Pro CCG Pro 30 GAC Asp	GAG Glu 15 CTC Leu ATC	GAA Glu GCG Ala TGT Cys	· W	96

### RAW SEQUENCE LISTING PATENT APPLICATION US/09/055,145A

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153 154 155	Pro	His 50	Arg	Phe	Ala	Pro	Leu 55	Ser	Asp	Gly	Ile	Leu 60	Val	Asn	Gly	His	
156	CTC	CAA	TGC	CCC	TAT	CAC	GGG	CTG	GAA	TTC	GAT	GGC	GGC	GGG	CAG	TGC	240
157	Leu	Gln	Cys	Pro	Tyr	His	Gly	Leu	Glu	Phe	Asp	Gly	Gly	Gly	Gln	Cys	
158	65					70					75					80	
159																	
160						GGC											288
161	Val	His	Asn	Pro	_	Gly	Asn	СТА	Ala	_	Pro	Ala	Ser	Leu		Val	
162					85					90					95		
163	aaa	maa	mma	aaa	ата	GTG	ana	aaa	a a a	aaa	аша	л Ш С	шаа	N III CI	таа	aaa	336
164 165						Val											336
166	ALG	Ser	rne	100	Val	Vai	GIU	ALG	105	AIG	пеп	116	тър	110	пр	FIO	
167				100					100								
168	GGC	GAT	CCG	GCG	CTG	GCC	GAT	CCT	GGG	GCG	ATC	CCC	GAC	TTC	GGC	TGC	384
169	Gly	Asp	Pro	Ala	Leu	Ala	Asp	Pro	Gly	Ala	Ile	Pro	Asp	Phe	Gly	Cys	
170			115					120					125				
171																	
172						TAT											432
173	Arg		Asp	Pro	Ala	Tyr	_	Thr	Val	Gly	Gly	_	Gly	His	Val	Asp	
174		130					135					140					
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179	113					130					100					100	
180	CAA	TAT	GTC	CAT	CGC	GCC	AAC	GCC	CAG	ACC	GAC	GCC	TTC	GAC	CGG	CTG	528
181	Gln	Tyr	Val	His	Arg	Ala	Asn	Ala	Gln	Thr	Asp	Ala	Phe	Asp	Arg	Leu	
182		-			165					170	_			_	175		
183																	
184						GTC											576
185	Glu	Arg	Glu		Ile	Val	Gly	Asp	_	Glu	Ile	Gln	Ala		Met	Lys	
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189						Pro											024
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191													- • -				
192	GCC	AAT	ACC	CCC	GTC	GAC	GCT	TGG	AAC	GAC	ATC	CGC	TGG	AAC	AAG	GTG	672
193	Ala	Asn	Thr	Pro	Val	Asp	Ala	Trp	Asn	Asp	Ile	Arg	Trp	Asn	Lys	Val	
194		210					215					220					
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197		АТА	мет	Leu	Asn	Phe	тте	АТа	vaı	АТА		GIU	стА	unr	Pro	-	
198 199	225					230					235					240	
200	GAG	CAG	ΔGC	ΔТС	CAC	TCG	CGC	GGT	ACC	САТ	ልጥሮ	ርሞር	ACC	כככ	GAG	ACG	768
201						Ser											, 00
202				= =	245		- 5	- 1		250					255		
203																	
204						TAT											816
205	Glu	Ala	Ser	Cys	His	Tyr	Phe	Phe	Gly	Ser	Ser	Arg	Asn	Phe	Gly	Ile	

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/055,145A

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206				260					265					270	,, 0,1		527450.147
207																	
208			CCG														864
209	Asp	Asp	Pro	Glu	Met	Asp	Gly	Val	Leu	Arg	Ser	Trp	Gln	Ala	Gln	Ala	
210			275					280					285				
211																	
212			AAG														912
213	Leu		Lys	Glu	Asp	Lys		Val	Val	Glu	Ala		Glu	Arg	Arg	Arg	
214		290					295					300					
215																~-~	242
216			GTC														960
217		Tyr	Val	GIU	Ala		GTÀ	TTe	Arg	Pro		мет	Leu	Ser	Cys	_	
218	305					310					315					320	
219	<b>a.</b> .	aaa	003	ama	aam	аша	N C C	aaa	ara	N III CI	ara	330	amm	ara	ara	ата	1000
220			GCA														1008
221 222	GIU	Ата	Ala	vaı	_	vaı	Ser	Arg	GIU		GIU	гуѕ	Leu	GIU		Leu	
222					325					330					335		
223	GAA	acc	GCC	TCA													1020
225		Ala		1 GA													1020
226	Giu	Ата	АТа	340													
227				340													
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234 235 236 237		·		(D)	) TOI	POLOC	GY: I	linea rote:	ar in			1:					
234 235 236 237 238	Met	(:		(D) MOLEC SEQUE	) TOI CULE ENCE	POLOG TYPI DESG	GY: ] E: pi	linea rote: rion	ar in : SE(	) ID	NO:		Leu	Pro	Glu	Glu	
234 235 236 237 238 239	Met 1	(:	кi) S	(D) MOLEC SEQUE	) TOI CULE ENCE	POLOG TYPI DESG	GY: ] E: pi	linea rote: rion	ar in : SE(	) ID	NO:		Leu	Pro	Glu 15	Glu	
234 235 236 237 238 239 240 241 242	1	(; Thr	xi) £	(D) MOLEG SEQUE Val	TOP CULE ENCE Arg 5	TYPI DESC Asn	GY: ] E: pr CRIPT	linea rote: FION Trp	ar in : SE(	) ID Val 10	NO:4	Ala			15		
234 235 236 237 238 239 240 241 242 243	1	(; Thr	кi) S	(D) MOLEC SEQUE Val	TOP CULE ENCE Arg 5	TYPI DESC Asn	GY: ] E: pr CRIPT	linea rote: FION Trp	ar in : SE( Tyr	) ID Val 10	NO:4	Ala		Pro	15		
234 235 236 237 238 239 240 241 242 243 244	1	(; Thr	xi) £	(D) MOLEG SEQUE Val	TOP CULE ENCE Arg 5	TYPI DESC Asn	GY: ] E: pr CRIPT	linea rote: FION Trp	ar in : SE(	) ID Val 10	NO:4	Ala			15		
234 235 236 237 238 239 240 241 242 243 244 245	l Leu	(: Thr Ser	Ri) S Phe Glu	(D) MOLEG SEQUE Val Lys 20	TOI CULE ENCE Arg 5	TYPH DESC Asn Leu	GY: I E: pr CRIPT Ala	linea rote: rION Trp Arg	in : SE( Tyr Thr 25	Q ID Val 10 Ile	NO:4	Ala Asp	Thr	Pro 30	15 Leu	Ala	
234 235 236 237 238 239 240 241 242 243 244 245 246	l Leu	(: Thr Ser	Phe Glu Arg	(D) MOLEG SEQUE Val Lys 20	TOI CULE ENCE Arg 5	TYPH DESC Asn Leu	GY: I E: pr CRIPT Ala	linearote: FION Trp Arg	in : SE( Tyr Thr 25	Q ID Val 10 Ile	NO:4	Ala Asp	Thr Leu	Pro 30	15 Leu	Ala	
234 235 236 237 238 239 240 241 242 243 244 245 246 247	l Leu	(: Thr Ser	Ri) S Phe Glu	(D) MOLEG SEQUE Val Lys 20	TOI CULE ENCE Arg 5	TYPH DESC Asn Leu	GY: I E: pr CRIPT Ala	linea rote: rION Trp Arg	in : SE( Tyr Thr 25	Q ID Val 10 Ile	NO:4	Ala Asp	Thr	Pro 30	15 Leu	Ala	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248	1 Leu Leu	Thr Ser Tyr	Phe Glu Arg 35	(D) MOLEG SEQUE Val Lys 20 Gln	TOI CULE ENCE Arg 5 Pro	TYPI  DESC  Asn  Leu  Asp	GY: CRIPTALA ALA GIY	linearote: FION Trp Arg Val 40	in : SE( Tyr Thr 25	Q ID Val 10 Ile	NO:4 Ala Leu	Ala Asp Leu	Thr Leu 45	Pro 30 Asp	15 Leu Ile	Ala Cys	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249	1 Leu Leu	Thr Ser Tyr	Phe Glu Arg	(D) MOLEG SEQUE Val Lys 20 Gln	TOI CULE ENCE Arg 5 Pro	TYPI  DESC  Asn  Leu  Asp	E: processor pro	linearote: FION Trp Arg Val 40	in : SE( Tyr Thr 25	Q ID Val 10 Ile	NO:4 Ala Leu	Ala Asp Leu	Thr Leu 45	Pro 30 Asp	15 Leu Ile	Ala Cys	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	1 Leu Leu	Thr Ser Tyr	Phe Glu Arg 35	(D) MOLEG SEQUE Val Lys 20 Gln	TOI CULE ENCE Arg 5 Pro	TYPI  DESC  Asn  Leu  Asp	GY: CRIPTALA ALA GIY	linearote: FION Trp Arg Val 40	in : SE( Tyr Thr 25	Q ID Val 10 Ile	NO:4 Ala Leu	Ala Asp Leu	Thr Leu 45	Pro 30 Asp	15 Leu Ile	Ala Cys	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	l Leu Leu Pro	Thr Ser Tyr His	Phe Glu Arg 35	(D) MOLEG SEQUE Val Lys 20 Gln Phe	DOI CULE ENCE Arg 5 Pro Pro	TYPI DESC Asn Leu Asp	E: processor pro	rote: FION Trp Arg Val 40	in : SE( Tyr Thr 25 Val	Val 10 1le Ala	NO:4 Ala Leu Ala Ile	Ala Asp Leu Leu	Thr Leu 45 Val	Pro 30 Asp	15 Leu Ile Gly	Ala Cys His	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252	Leu Pro Leu	Thr Ser Tyr His	Phe Glu Arg 35	(D) MOLEG SEQUE Val Lys 20 Gln Phe	DOI CULE ENCE Arg 5 Pro Pro	TYPI DESC Asn Leu Asp Pro	E: processor pro	rote: FION Trp Arg Val 40	in : SE( Tyr Thr 25 Val	Val 10 1le Ala	NO:4 Ala Leu Ala Ile Asp	Ala Asp Leu Leu	Thr Leu 45 Val	Pro 30 Asp	15 Leu Ile Gly	Ala Cys His	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253	l Leu Leu Pro	Thr Ser Tyr His	Phe Glu Arg 35	(D) MOLEG SEQUE Val Lys 20 Gln Phe	DOI CULE ENCE Arg 5 Pro Pro	TYPI DESC Asn Leu Asp	E: processor pro	rote: FION Trp Arg Val 40	in : SE( Tyr Thr 25 Val	Val 10 1le Ala	NO:4 Ala Leu Ala Ile	Ala Asp Leu Leu	Thr Leu 45 Val	Pro 30 Asp	15 Leu Ile Gly	Ala Cys His	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254	Leu Pro Leu 65	Thr Ser Tyr His 50	Phe Glu Arg 35 Arg	(D) MOLEG SEQUE Val Lys 20 Gln Phe	TOI CULE ENCE Arg 5 Pro Pro Ala	TYPI DESC Asn Leu Asp Pro His 70	E: processor pro	linearote: FION Trp Arg Val 40 Ser	in : SE( Tyr Thr 25 Val Asp	Val 10 Ile Ala Gly	NO:4 Ala Leu Ala Ile Asp 75	Ala Asp Leu 60	Thr Leu 45 Val	Pro 30 Asp Asn	15 Leu Ile Gly	Ala Cys His Cys	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255	Leu Pro Leu 65	Thr Ser Tyr His 50	Phe Glu Arg 35	(D) MOLEG SEQUE Val Lys 20 Gln Phe	TOI CULE ENCE Arg 5 Pro Pro Ala Tyr	TYPI DESC Asn Leu Asp Pro His 70	E: processor pro	linearote: FION Trp Arg Val 40 Ser	in : SE( Tyr Thr 25 Val Asp	Val 10 Ile Ala Gly Phe	NO:4 Ala Leu Ala Ile Asp 75	Ala Asp Leu 60	Thr Leu 45 Val	Pro 30 Asp Asn	15 Leu Ile Gly Gln Asn	Ala Cys His Cys	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256	Leu Pro Leu 65	Thr Ser Tyr His 50	Phe Glu Arg 35 Arg	(D) MOLEG SEQUE Val Lys 20 Gln Phe	TOI CULE ENCE Arg 5 Pro Pro Ala	TYPI DESC Asn Leu Asp Pro His 70	E: processor pro	linearote: FION Trp Arg Val 40 Ser	in : SE( Tyr Thr 25 Val Asp	Val 10 Ile Ala Gly	NO:4 Ala Leu Ala Ile Asp 75	Ala Asp Leu 60	Thr Leu 45 Val	Pro 30 Asp Asn	15 Leu Ile Gly	Ala Cys His Cys	
234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255	Leu Pro Leu 65	Thr Ser Tyr His 50 Gln His	Phe Glu Arg 35 Arg	(D) MOLEG SEQUE Val Lys 20 Gln Phe Pro	TOI CULE ENCE Arg 5 Pro Pro Ala Tyr	TYPI DESC Asn Leu Asp Pro His 70 Gly	E: processor pro	linearote: FION Trp Arg Val 40 Ser Leu Gly	in : SE( Tyr Thr 25 Val Asp Glu Ala	Val 10 Ile Ala Gly Phe Arg 90	NO:4 Ala Leu Ala Ile Asp 75	Ala Asp Leu 60 Gly Ala	Thr Leu 45 Val Gly Ser	Pro 30 Asp Asn Gly	15 Leu Ile Gly Gln Asn 95	Ala Cys His Cys 80 Val	

## **SEQUENCE VERIFICATION REPORT** PATENT APPLICATION *US/09/055,145A*

DATE: 10/26/98 TIME: 11:25:17

INPUT SET: S29430.raw

Line Error Original Text

303 Stop Codon at end of sequence removed - no error 389 Stop Codon at end of sequence removed - no error